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119

SEQUENCE LISTING

T, 0870

(1) GENERAL INFORMATION:

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(ii) TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS

(iii) NUMBER OF SEQUENCES: 113

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/634,278  
(B) FILING DATE: 19-DEC-1990  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

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(B) FILING DATE: 28-SEP-1990

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/310,252  
(B) FILING DATE: 13-FEB-1989

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/290,975  
(B) FILING DATE: 28-DEC-1988

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(C) REFERENCE/DOCKET NUMBER: 11823-002600

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SEP 14 1998  
GROUP 2100

87

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120

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..106
- (D) OTHER INFORMATION: /note= "Variable region of the mouse anti-Tac antibody light chain."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

F1

Gln	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Ile	Met	Ser	Ala	Ser	Pro	Gly
1				5					10					15	
Glu	Lys	Val	Thr	Ile	Thr	Cys	Ser	Ala	Ser	Ser	Ser	Ile	Ser	Tyr	Met
			20					25					30		
His	Trp	Phe	Gln	Gln	Lys	Pro	Gly	Thr	Ser	Pro	Lys	Leu	Trp	Ile	Tyr
		35					40					45			
Thr	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser
	50					55					60				
Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile	Ser	Arg	Met	Glu	Ala	Glu
65					70					75					80
Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	His	Gln	Arg	Ser	Thr	Tyr	Pro	Leu	Thr
				85					90					95	
Phe	Gly	Ser	Gly	Thr	Lys	Leu	Glu	Leu	Lys						
			100					105							

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..107
- (D) OTHER INFORMATION: /note= "Variable region of the human Eu antibody light chain."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly  
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asn Thr Trp  
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Met  
35 40 45

Tyr Lys Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ile Gly  
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Asp Ser Lys  
85 90 95

Met Phe Gly Gln Gly Thr Lys Val Glu Val Lys  
100 105

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..116
- (D) OTHER INFORMATION: /note= "Variable region of the mouse anti-Tac antibody heavy chain."

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122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Ala	Lys	Pro	Gly	Ala	
1				5					10					15		
Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr	
			20					25					30			
Arg	Met	His	Trp	Val	Lys	Gln	Arg	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile	
		35					40					45				
Gly	Tyr	Ile	Asn	Pro	Ser	Thr	Gly	Tyr	Thr	Glu	Tyr	Asn	Gln	Lys	Phe	
	50					55					60					
Lys	Asp	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr	
65					70					75					80	
Met	Gln	Leu	Ser	Ser	Leu	Thr	Phe	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys	
				85					90					95		
Ala	Arg	Gly	Gly	Gly	Val	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Leu	
			100					105					110			
Thr	Val	Ser	Ser													
			115													

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..117
- (D) OTHER INFORMATION: /note= "Variable region of the human Eu antibody heavy chain."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ser	
1				5					10					15		
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Gly	Thr	Phe	Ser	Arg	Ser	
			20					25					30			

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Ala	Ile	Ile	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
		35					40					45			
Gly	Gly	Ile	Val	Pro	Met	Phe	Gly	Pro	Pro	Asn	Tyr	Ala	Gln	Lys	Phe
	50					55					60				
Gln	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Glu	Ser	Thr	Asn	Thr	Ala	Tyr
65					70					75					80
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Phe	Tyr	Phe	Cys
				85					90					95	
Ala	Gly	Gly	Tyr	Gly	Ile	Tyr	Ser	Pro	Glu	Glu	Tyr	Asn	Gly	Gly	Leu
			100					105					110		
Val	Thr	Val	Ser	Ser											

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..116
- (D) OTHER INFORMATION: /note= "Variable region of the PDL humanized anti-Tac antibody heavy chain."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ser
1				5					10					15	
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr
			20					25					30		
Arg	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile
		35					40					45			
Gly	Tyr	Ile	Asn	Pro	Ser	Thr	Gly	Tyr	Thr	Glu	Tyr	Asn	Gln	Lys	Phe
	50					55					60				
Lys	Asp	Lys	Ala	Thr	Ile	Thr	Ala	Asp	Glu	Ser	Thr	Asn	Thr	Ala	Tyr
65					70					75					80

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124

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95  
Ala Arg Gly Gly Gly Val Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val  
100 105 110  
Thr Val Ser Ser  
115

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..116
- (D) OTHER INFORMATION: /note= "Variable region of the CDR-only humanized anti-Tac antibody heavy chain."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser  
1 5 10 15  
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr  
20 25 30  
Arg Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
35 40 45  
Gly Tyr Ile Asn Pro Ser Thr Gly Tyr Thr Glu Tyr Asn Gln Lys Phe  
50 55 60  
Lys Asp Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr  
65 70 75 80  
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe Tyr Phe Cys  
85 90 95  
Ala Gly Gly Gly Gly Val Phe Asp Tyr Glu Tyr Asn Gly Gly Leu Val  
100 105 110  
Thr Val Ser Ser  
115

92

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125

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..106
- (D) OTHER INFORMATION: /note= "Variable region of the PDL humanized anti-Tac antibody light chain."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

F<sub>1</sub>

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Thr	Leu	Ser	Ala	Ser	Val	Gly	
1				5					10					15		
Asp	Arg	Val	Thr	Ile	Thr	Cys	Ser	Ala	Ser	Ser	Ser	Ile	Ser	Tyr	Met	
			20					25					30			
His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	
			35				40					45				
Thr	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	
			50			55					60					
Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Asp	
65				70						75					80	
Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	His	Gln	Arg	Ser	Thr	Tyr	Pro	Leu	Thr	
				85					90					95		
Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Val	Lys							
			100					105								

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

93

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~~126~~

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: Protein

(B) LOCATION: 1..106

(D) OTHER INFORMATION: /note= "Variable region of the CDR-only humanized anti-Tac antibody light chain."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly  
1 5 10 15  
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Ile Ser Tyr Met  
20 25 30  
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Met Tyr  
35 40 45  
Thr Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ile Gly Ser  
50 55 60  
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp  
65 70 75 80  
F<sub>1</sub> Asp Phe Ala Thr Tyr Tyr Cys His Gln Arg Ser Thr Tyr Pro Leu Thr  
85 90 95  
Phe Gly Gln Gly Thr Lys Val Glu Val Lys  
100 105

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 443 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1..443

(D) OTHER INFORMATION: /note= "Sequence encoding heavy chain variable region of CDR-only humanized anti-Tac antibody including signal sequence."

94



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127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AGCTTCTAGA TGGGATGGAG CTGGATCTTT CTCTTCCTCC TGTCAGGTAC CGCGGGCGTG	60
CACTCTCAGG TCCAGCTTGT CCAGTCTGGG GCTGAAGTCA AGAAACCTGG CTCGAGCGTG	120
AAGGTCTCCT GCAAGGCTTC TGGCGGGACC TTTTCTAGCT ACAGGATGCA CTGGGTAAGG	180
CAGGCCCCCTG GACAGGGTCT GGAATGGATG GGATATATTA ATCCGTCGAC TGGGTATACT	240
GAATACAATC AGAAGTTCAA GGACAGGGTC ACAATTACTG CAGACGAATC CACCAATACA	300
GCCTACATGG AACTGAGCAG CCTGAGATCT GAGGACACCG CATTCTATTT CTGTGCAGGG	360
GGTGGGGGAG TCTTTGACTA CGAATACAAT GGAGGGCTGG TCACAGTCTC CTCAGGTGAG	420
TCCTTAAAC CTCTAGACGA TAT	443

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

F1

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..411
- (D) OTHER INFORMATION: /note= "Sequence encoding light chain variable region of the CDR-only humanized anti-Tac antibody including signal sequence."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CAAATCTAGA TGGAGACCGA TACCCTCCTG CTATGGGTCC TCCTGCTATG GGTCCCAGGA	60
TCAACCGGAG ATATTCAGAT GACCCAGTCT CCATCTACCC TCTCTGCTAG CGTCGGGGAT	120
AGGGTCACCA TAACCTGCTC TGCCAGCTCA AGTATAAGTT ACATGCACTG GTACCAGCAG	180
AAGCCAGGCA AAGCTCCCAA GCTTCTAATG TATACCACAT CCAACCTGGC TTCTGGAGTC	240
CCTTCTCGCT TCATTGGCAG TGGATCTGGG ACCGAGTTCA CCCTCACAAT CAGCTCTCTG	300
CAGCCAGATG ATTTGCGCCAC TTATTACTGC CATCAAAGGA GTACTTACCC ACTCACGTTC	360
GGTCAGGGGA CCAAGGTGGA GGTCAAACGT AAGTACACTT TTCTAGATAT A	411

95

95  
128

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..29
- (D) OTHER INFORMATION: /standard\_name= "Primer mc045"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TAATCTAGAA TTCCCCCCCC CCCCCCCC

29

(2) INFORMATION FOR SEQ ID NO:12:

F1 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..46
- (D) OTHER INFORMATION: /standard\_name= "Primer mc045"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TATAGAGCTC AAGCTTGGAT GGTGGGAAGA TGGATACAGT TGGTGC

46

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid

96

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129

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1..50

(D) OTHER INFORMATION: /standard\_name= "Primer mc047"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TATAGAGCTC AAGCTTCCAG TGGATAGACH GATGGGGSTG TYGTTTTGGC

50

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

F1

(ix) FEATURE:

(A) NAME/KEY: Protein

(B) LOCATION: 1..116

(D) OTHER INFORMATION: /note= "Anti-Tac heavy chain amino acid sequence."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Lys Pro Gly Ala  
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
20 25 30

Arg Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile  
35 40 45

Gly Tyr Ile Asn Pro Ser Thr Gly Tyr Thr Glu Tyr Asn Gln Lys Phe  
50 55 60

Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr  
65 70 75 80

97

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130

Met	Gln	Leu	Ser	Ser	Leu	Thr	Phe	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Ala	Arg	Gly	Gly	Gly	Val	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Leu
			100					105					110		
Thr	Val	Ser	Ser												
			115												

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..117
- (D) OTHER INFORMATION: /note= "Eu heavy chain amino acid sequence."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

F<sub>1</sub>

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ser
1				5					10					15	
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Gly	Thr	Phe	Ser	Arg	Ser
			20					25					30		
Ala	Ile	Ile	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
		35					40					45			
Gly	Gly	Ile	Val	Pro	Met	Phe	Gly	Pro	Pro	Asn	Tyr	Ala	Gln	Lys	Phe
	50					55					60				
Gln	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Glu	Ser	Thr	Asn	Thr	Ala	Tyr
65					70					75					80
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Phe	Tyr	Phe	Cys
				85					90					95	
Ala	Gly	Gly	Tyr	Gly	Ile	Tyr	Ser	Pro	Glu	Glu	Tyr	Asn	Gly	Gly	Leu
			100					105					110		
Val	Thr	Val	Ser	Ser											
			115												

98

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131

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..106
- (D) OTHER INFORMATION: /note= "Anti-Tac light chain amino acid sequence."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly  
1 5 10 15  
Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Ile Ser Tyr Met  
20 25 30  
His Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro Lys Leu Trp Ile Tyr  
35 40 45  
F1 Thr Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser  
50 55 60  
Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu Ala Glu  
65 70 75 80  
Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg Ser Thr Tyr Pro Leu Thr  
85 90 95  
Phe Gly Ser Gly Thr Lys Leu Glu Leu Lys  
100 105

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

99

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132

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..107
- (D) OTHER INFORMATION: /note= "Eu light chain amino acid sequence."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly  
1 5 10 15  
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asn Thr Trp  
20 25 30  
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Met  
35 40 45  
Tyr Lys Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ile Gly  
50 55 60  
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80  
Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Asp Ser Lys  
85 90 95  
F1 Met Phe Gly Gln Gly Thr Lys Val Glu Val Lys  
100 105

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 6..410
- (D) OTHER INFORMATION: /product= "Humanized anti-Tac heavy chain variable region, Seq ID. 19"

100

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TCTAG ATG GGA TGG AGC TGG ATC TTT CTC TTC CTC CTG TCA GGT ACC	47
Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr	
1 5 10	
GCG GGC GTG CAC TCT CAG GTC CAG CTT GTC CAG TCT GGG GCT GAA GTC	95
Ala Gly Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val	
15 20 25 30	
AAG AAA CCT GGC TCG AGC GTG AAG GTC TCC TGC AAG GCT TCT GGC TAC	143
Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr	
35 40 45	
ACC TTT ACT AGC TAC AGG ATG CAC TGG GTA AGG CAG GCC CCT GGA CAG	191
Thr Phe Thr Ser Tyr Arg Met His Trp Val Arg Gln Ala Pro Gly Gln	
50 55 60	
GGT CTG GAA TGG ATT GGA TAT ATT AAT CCG TCG ACT GGG TAT ACT GAA	239
Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Thr Gly Tyr Thr Glu	
65 70 75	
TAC AAT CAG AAG TTC AAG GAC AAG GCA ACA ATT ACT GCA GAC GAA TCC	287
Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Ile Thr Ala Asp Glu Ser	
80 85 90	
ACC AAT ACA GCC TAC ATG GAA CTG AGC AGC CTG AGA TCT GAG GAC ACC	335
Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr	
95 100 105 110	
GCA GTC TAT TAC TGT GCA AGA GGG GGG GGG GTC TTT GAC TAC TGG GGC	383
Ala Val Tyr Tyr Cys Ala Arg Gly Gly Gly Val Phe Asp Tyr Trp Gly	
115 120 125	
CAA GGA ACC CTG GTC ACA GTC TCC TCA GGTGAGTCCT TAAAACCTCT	430
Gln Gly Thr Leu Val Thr Val Ser Ser	
130 135	
AGA	433

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
1 5 10 15

101

101  
134

Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys
			20					25					30		
Pro	Gly	Ser	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe
		35					40					45			
Thr	Ser	Tyr	Arg	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu
	50					55					60				
Glu	Trp	Ile	Gly	Tyr	Ile	Asn	Pro	Ser	Thr	Gly	Tyr	Thr	Glu	Tyr	Asn
65					70					75					80
Gln	Lys	Phe	Lys	Asp	Lys	Ala	Thr	Ile	Thr	Ala	Asp	Glu	Ser	Thr	Asn
				85					90					95	
Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val
			100					105					110		
Tyr	Tyr	Cys	Ala	Arg	Gly	Gly	Gly	Val	Phe	Asp	Tyr	Trp	Gly	Gln	Gly
		115					120					125			
Thr	Leu	Val	Thr	Val	Ser	Ser									
130						135									

(2) INFORMATION FOR SEQ ID NO:20:

F1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 6..383
- (D) OTHER INFORMATION: /product= "Humanized anti-Tac light chain variable region: Seq ID. 21"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TCTAG	ATG	GAG	ACC	GAT	ACC	CTC	CTG	CTA	TGG	GTC	CTC	CTG	CTA	TGG	47
Met	Glu	Thr	Asp	Thr	Leu	Leu	Leu	Trp	Val	Leu	Leu	Leu	Trp		
1				5				10							
GTC	CCA	GGA	TCA	ACC	GGA	GAT	ATT	CAG	ATG	ACC	CAG	TCT	CCA	TCT	ACC
Val	Pro	Gly	Ser	Thr	Gly	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Thr
15				20				25					30		95

102



102  
135

CTC	TCT	GCT	AGC	GTC	GGG	GAT	AGG	GTC	ACC	ATA	ACC	TGC	TCT	GCC	AGC	143
Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Ser	Ala	Ser	
				35					40					45		
TCA	AGT	ATA	AGT	TAC	ATG	CAC	TGG	TAC	CAG	CAG	AAG	CCA	GGC	AAA	GCT	191
Ser	Ser	Ile	Ser	Tyr	Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	
			50					55					60			
CCC	AAG	CTT	CTA	ATT	TAT	ACC	ACA	TCC	AAC	CTG	GCT	TCT	GGA	GTC	CCT	239
Pro	Lys	Leu	Leu	Ile	Tyr	Thr	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	
		65					70					75				
GCT	CGC	TTC	AGT	GGC	AGT	GGA	TCT	GGG	ACC	GAG	TTC	ACC	CTC	ACA	ATC	287
Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	
	80					85					90					
AGC	TCT	CTG	CAG	CCA	GAT	GAT	TTC	GCC	ACT	TAT	TAC	TGC	CAT	CAA	AGG	335
Ser	Ser	Leu	Gln	Pro	Asp	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	His	Gln	Arg	
	95				100				105					110		
AGT	ACT	TAC	CCA	CTC	ACG	TTC	GGT	CAG	GGG	ACC	AAG	GTG	GAG	GTC	AAA	383
Ser	Thr	Tyr	Pro	Leu	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Val	Lys	
				115				120					125			
CGTAAGTACA	CTTTTCTAGA															403

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 126 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met	Glu	Thr	Asp	Thr	Leu	Leu	Leu	Trp	Val	Leu	Leu	Leu	Trp	Val	Pro	
1				5					10					15		
Gly	Ser	Thr	Gly	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Thr	Leu	Ser	
			20				25						30			
Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Ser	Ala	Ser	Ser	Ser	
		35					40					45				
Ile	Ser	Tyr	Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	
	50					55					60					
Leu	Leu	Ile	Tyr	Thr	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Ala	Arg	
65					70					75					80	

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136

Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser  
85 90 95  
Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys His Gln Arg Ser Thr  
100 105 110  
Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys  
115 120 125

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..126
- (D) OTHER INFORMATION: /standard\_name= "Oligo HES12"  
/note= "One of four oligonucleotides used to  
synthesize the humanized anti-Tac heavy chain  
gene."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AGCTTCTAGA TGGGATGGAG CTGGATCTTT CTCTTCCTCC TGTCAGGTAC CGCGGGCGTG 60  
CACTCTCAGG TCCAGCTTGT CCAGTCTGGG GCTGAAGTCA AGAAACCTGG CTCGAGCGTG 120  
AAGGTC 126

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

104

104  
137

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: /standard\_name= "Oligo HES13"  
/note= "One of four oligonucleotides used to  
synthesize the humanized anti-Tac heavy chain  
gene."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CCCAGTCGAC GGATTAATAT ATCCAATCCA TTCCAGACCC TGTCCAGGGG CCTGCCTTAC	60
CCAGTGCATC CTGTAGCTAG TAAAGGTGTA GCCAGAAGCC TTGCAGGAGA CCTTCACGCT	120
CGAGCCAGG	129

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

F<sub>1</sub>

- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..124
- (D) OTHER INFORMATION: /standard\_name= "Oligo HES14"  
/note= "One of four oligonucleotides used to  
synthesize the humanized anti-Tac heavy chain  
gene."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TATATTAATC CGTCGACTGG GTATACTGAA TACAATCAGA AGTTCAAGGA CAAGGCAACA	60
ATTACTGCAG ACGAATCCAC CAATACAGCC TACATGGAAC TGAGCAGCCT GAGATCTGAG	120
GACA	124

105

105  
128

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..128
- (D) OTHER INFORMATION: /standard\_name= "Oligo HES15"  
/note= "One of four oligonucleotides used to  
synthesize the humanized anti-Tac heavy chain  
gene."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATATCGTCTA GAGGTTTAA GGACTCACCT GAGGAGACTG TGACCAGGGT TCCTTGGCCC 60  
CAGTAGTCAA AGACCCCCCC CCCTCTTGCA CAGTAATAGA CTGCGGTGTC CTCAGATCTC 120  
AGGCTGCT 128

F<sub>1</sub>

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: /standard\_name= "Oligo JFD1"  
/note= "One of four oligonucleotides used to  
synthesize the humanized anti-Tac light chain  
gene."

106

106  
139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CAAATCTAGA TGGAGACCGA TACCCTCCTG CTATGGGTCC TCCTGCTATG GGTCCCAGGA	60
TCAACCGGAG ATATTCAGAT GACCCAGTCT CCATCTACCC TCTCTGCTAG CGTCGGGGAT	120

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..114
- (D) OTHER INFORMATION: /standard\_name= "Oligo JFD2"  
/note= "One of four oligonucleotides used to  
synthesize the humanized anti-Tac light chain  
gene."

F<sub>1</sub>

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATAAATTAGA AGCTTGGGAG CTTTGCCTGG CTTCTGCTGG TACCAGTGCA TGTAAGTTAT	60
ACTTGAGCTG GCAGAGCAGG TTATGGTGAC CCTATCCCCG ACGCTAGCAG AGAG	114

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature

107

- (B) LOCATION: 1..123  
 (D) OTHER INFORMATION: /standard\_name= "Oligo JFD3"  
 /note= "One of four oligonucleotides used to  
 synthesize the humanized anti-Tac light chain  
 gene."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GCTCCCAAGC TTCTAATTTA TACCACATCC AACCTGGCTT CTGGAGTCCC TGCTCGCTTC	60
AGTGGCAGTG GATCTGGGAC CGAGTTCACC CTCACAATCA GCTCTCTGCA GCCAGATGAT	120
TTC	123

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..122
- (D) OTHER INFORMATION: /standard\_name= "Oligo JFD4"  
 /note= "One of four oligonucleotides used to  
 synthesize the humanized anti-Tac light chain  
 gene."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TATATCTAGA AAAGTGTACT TACGTTTGAC CTCCACCTTG GTCCCCTGAC CGAACGTGAG	60
TGGGTAAGTA CTCCTTTGAT GGCAGTAATA AGTGGCGAAA TCATCTGGCT GCAGAGAGCT	120
GA	122

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid

108

108  
141

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..384

(D) OTHER INFORMATION: /product= "Light chain variable region of mik-beta1: Seq ID No. 31"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATG	GAT	TTT	CAA	GTG	CAG	ATT	TTC	AGC	TTC	CTG	CTA	ATC	AGT	GCC	TCA	48
Met	Asp	Phe	Gln	Val	Gln	Ile	Phe	Ser	Phe	Leu	Leu	Ile	Ser	Ala	Ser	
1				5				10						15		
GTC	ATA	CTG	TCC	AGA	GGA	CAA	ATT	GTT	CTC	ACC	CAG	TCT	CCA	GCA	ATC	96
Val	Ile	Leu	Ser	Arg	Gly	Gln	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Ile	
			20					25					30			
ATG	TCT	GCG	TCT	CCA	GGG	GAG	AAG	GTC	ACC	ATG	ACC	TGC	AGT	GGC	AGC	144
Met	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Ser	Gly	Ser	
		35					40					45				
TCA	AGT	GTA	AGT	TTC	ATG	TAC	TGG	TAC	CAG	CAG	AGG	CCA	GGA	TCC	TCC	192
Ser	Ser	Val	Ser	Phe	Met	Tyr	Trp	Tyr	Gln	Gln	Arg	Pro	Gly	Ser	Ser	
	50					55					60					
CCC	AGA	CTC	CTG	ATT	TAT	GAC	ACA	TCC	AAC	CTG	GCT	TCT	GGA	GTC	CCT	240
Pro	Arg	Leu	Leu	Ile	Tyr	Asp	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	
65				70						75					80	
GTT	CGC	TTC	AGT	GGC	AGT	GGG	TCT	GGG	ACC	TCT	TAC	TCT	CTC	ACA	ATC	288
Val	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile	
			85					90					95			
AGC	CGA	ATG	GAG	GCT	GAA	GAT	GCT	GCC	ACT	TAT	TAC	TGC	CAG	CAG	TGG	336
Ser	Arg	Met	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp	
			100					105					110			
AGT	ACT	TAC	CCG	CTC	ACG	TTC	GGT	GCT	GGG	ACC	AAG	CTG	GAG	CTG	AAA	384
Ser	Thr	Tyr	Pro	Leu	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys	
		115					120					125				

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

109

169  
142

(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
1 5 10 15  
Val Ile Leu Ser Arg Gly Gln Ile Val Leu Thr Gln Ser Pro Ala Ile  
20 25 30  
Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Gly Ser  
35 40 45  
Ser Ser Val Ser Phe Met Tyr Trp Tyr Gln Gln Arg Pro Gly Ser Ser  
50 55 60  
Pro Arg Leu Leu Ile Tyr Asp Thr Ser Asn Leu Ala Ser Gly Val Pro  
65 70 75 80  
Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
85 90 95  
Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
100 105 110  
Ser Thr Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
115 120 125

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..414
- (D) OTHER INFORMATION: /product= "Heavy chain var. region  
of the antibody mik-beta1: SeqID 33"

110



110  
143

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ATG	GCT	GTC	TTG	GGG	CTG	CTC	TTC	TGC	CTG	GTG	ACA	TTC	CCA	AGC	TGT	48
Met	Ala	Val	Leu	Gly	Leu	Leu	Phe	Cys	Leu	Val	Thr	Phe	Pro	Ser	Cys	
1				5					10					15		
GTC	CTA	TCC	CAG	GTG	CAG	CTG	AAG	CAG	TCA	GGA	CCT	GGC	CTA	GTG	CAG	96
Val	Leu	Ser	Gln	Val	Gln	Leu	Lys	Gln	Ser	Gly	Pro	Gly	Leu	Val	Gln	
			20					25					30			
CCC	TCA	CAG	AGC	CTG	TCC	ATC	ACC	TGC	ACA	GTC	TCT	GGT	TTC	TCA	GTA	144
Pro	Ser	Gln	Ser	Leu	Ser	Ile	Thr	Cys	Thr	Val	Ser	Gly	Phe	Ser	Val	
		35					40					45				
ACA	AGT	TAT	GGT	GTA	CAC	TGG	ATT	CGC	CAG	TCT	CCA	GGA	AAG	GGT	CTG	192
Thr	Ser	Tyr	Gly	Val	His	Trp	Ile	Arg	Gln	Ser	Pro	Gly	Lys	Gly	Leu	
	50					55					60					
GAG	TGG	CTG	GGA	GTG	ATA	TGG	AGT	GGT	GGA	AGC	ACA	GAC	TAT	AAT	GCA	240
Glu	Trp	Leu	Gly	Val	Ile	Trp	Ser	Gly	Gly	Ser	Thr	Asp	Tyr	Asn	Ala	
65					70				75						80	
GCT	TTC	ATA	TCC	AGA	CTG	ACC	ATC	AGC	AAG	GAC	AAC	TCC	AAG	AGC	CAA	288
Ala	Phe	Ile	Ser	Arg	Leu	Thr	Ile	Ser	Lys	Asp	Asn	Ser	Lys	Ser	Gln	
				85					90					95		
GTT	TTC	TTT	AAA	GTG	AAC	AGT	CTG	CAA	CCT	GCT	GAC	ACA	GCC	ATA	TAC	336
Val	Phe	Phe	Lys	Val	Asn	Ser	Leu	Gln	Pro	Ala	Asp	Thr	Ala	Ile	Tyr	
			100					105					110			
TAT	TGT	GCC	AGA	GCT	GGG	GAC	TAT	AAT	TAC	GAC	GGT	TTT	GCT	TAC	TGG	384
Tyr	Cys	Ala	Arg	Ala	Gly	Asp	Tyr	Asn	Tyr	Asp	Gly	Phe	Ala	Tyr	Trp	
		115					120					125				
GGC	CAA	GGG	ACT	CTG	GTC	ACT	GTC	TCT	GCG							414
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ala							
		130					135									

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met Ala Val Leu Gly Leu Leu Phe Cys Leu Val Thr Phe Pro Ser Cys  
1 5 10 15

|||

144

Val Leu Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln  
 20 25 30  
 Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Val  
 35 40 45  
 Thr Ser Tyr Gly Val His Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu  
 50 55 60  
 Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Ser Thr Asp Tyr Asn Ala  
 65 70 75 80  
 Ala Phe Ile Ser Arg Leu Thr Ile Ser Lys Asp Asn Ser Lys Ser Gln  
 85 90 95  
 Val Phe Phe Lys Val Asn Ser Leu Gln Pro Ala Asp Thr Ala Ile Tyr  
 100 105 110  
 Tyr Cys Ala Arg Ala Gly Asp Tyr Asn Tyr Asp Gly Phe Ala Tyr Trp  
 115 120 125  
 Gly Gln Gly Thr Leu Val Thr Val Ser Ala  
 130 135

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: Protein  
 (B) LOCATION: 1..107  
 (D) OTHER INFORMATION: /note= "Amino acid sequence of the light chain for humane Lay antibody."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Val Ser Val Gly  
 1 5 10 15  
 Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asn Val Asn Ala Tyr  
 20 25 30  
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Leu Ala Pro Lys Leu Leu Ile  
 35 40 45

112

112  
145

Tyr Gly Ala Ser Thr Arg Glu Ala Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60  
Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80  
Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Asn Trp Pro Pro  
85 90 95  
Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys  
100 105

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 106 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: Protein  
 (B) LOCATION: 1..106  
 (D) OTHER INFORMATION: /note= "Amino acid sequence of the  
 light chain of the humanized mik-beta1 antibody."

F1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15  
Asp Arg Val Thr Ile Thr Cys Ser Gly Ser Ser Ser Val Ser Phe Met  
20 25 30  
Tyr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr  
35 40 45  
Asp Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser  
50 55 60  
Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu  
65 70 75 80  
Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Thr Tyr Pro Leu Thr  
85 90 95  
Phe Gly Gln Gly Thr Lys Val Glu Val Lys  
100 105

113

113  
146

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..122
- (D) OTHER INFORMATION: /note= "Amino acid sequence of the heavy chain of the human Lay antibody."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Ala Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Ser  
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ala Trp Lys Tyr Glu Asn Gly Asn Asp Lys His Tyr Ala Asp Ser Val  
50 55 60

Asn Gly Arg Phe Thr Ile Ser Arg Asn Asp Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Gly Leu Gln Ala Glx Val Ser Ala Ile Tyr Tyr Cys  
85 90 95

Ala Arg Asp Ala Gly Pro Tyr Val Ser Pro Thr Phe Phe Ala His Trp  
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
115 120

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

114

114  
147

- (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:
- (A) NAME/KEY: Protein
  - (B) LOCATION: 1..119
  - (D) OTHER INFORMATION: /note= "Amino acid sequence of the heavy chain of the humanized mik-betal antibody."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

F1

Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	
1				5					10					15		
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Val	Thr	Ser	Tyr	
			20					25					30			
Gly	Val	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
		35				40						45				
Gly	Val	Ile	Trp	Ser	Gly	Gly	Ser	Thr	Asp	Tyr	Asn	Ala	Ala	Phe	Ile	
		50				55					60					
Ser	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	Leu	
65					70					75					80	
Gln	Met	Asn	Ser	Leu	Gln	Ala	Glu	Asp	Thr	Ala	Ile	Tyr	Tyr	Cys	Ala	
				85					90					95		
Arg	Ala	Gly	Asp	Tyr	Asn	Tyr	Asp	Gly	Phe	Ala	Tyr	Trp	Gly	Gln	Gly	
			100					105					110			
Thr	Leu	Val	Thr	Val	Ser	Ser										

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 107 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO

115

15  
148

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..107
- (D) OTHER INFORMATION: /standard\_name= "Oligo vc13"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TTCTGCTGGT ACCAGTACAT GAAACTTACA CTTGAGCTGC CACTGCAGGT GATGGTGACG	60
CGGTCACCCA CTGAGGCACT GAGGCTAGAT GGAGACTGGG TCATTTG	107

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

F (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: /standard\_name= "Oligo vc14"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CATGTACTGG TACCAGCAGA AGCCAGGAAA AGCTCCGAAA CTTCTGATTT ATGACACATC	60
CAACCTGGCT TCTGGAGTCC CTTCCCGCTT CAGTGGCAGT GGGTCTGGGA CCGATTACAC	120
CTTTACAATC TCTTCA	136

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

106

116  
~~149~~

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..137
- (D) OTHER INFORMATION: /standard\_name= "Oligo vc15"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TGTGTCTAGA AAAGTGTACT TACGTTTTAC CTCGACCTTG GTCCCTTGAC CGAACGTGAG	60
CGGGTAAGTA CTCCACTGCT GGCAGTAATA AGTGGCTATA TCTTCCGGCT GAAGTGAAGA	120
GATTGTAAAG GTGTAAT	137

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

F1 (ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..108
- (D) OTHER INFORMATION: /standard\_name= "Oligo vc16"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CACATCTAGA CCACCATGGA TTTTCAAGTG CAGATCTTCA GCTTCCTGCT AATCAGTGCC	60
TCAGTCATAC TGTCCAGAGG AGATATTCAA ATGACCCAGT CTCCATCT	108

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

117

117  
150

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1..138

(D) OTHER INFORMATION: /standard\_name= "Oligo vc11"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TAGTCTGTCG ACCCACCCT CCATATCACT CCCACCCACT CGAGTCCCTT TCCAGGAGCC	60
TGGCGGACCC AGTGTACACC ATAACCTGTT ACGGTGAAAC CACTGGCGGC ACAAGACAGT	120
CTCAGAGATC CTCCTGGC	138

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

F (ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1..126

(D) OTHER INFORMATION: /standard\_name= "Oligo vc12"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TGGTGGGTCG ACAGACTATA ATGCAGCTTT CATATCCAGA TTTACCATCA GCAGAGACAA	60
CAGCAAGAAC ACACTGTATC TCCAAATGAA TAGCCTGCAA GCCGAGGACA CAGCCATATA	120
TTATTG	126

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 base pairs

118



118  
131

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..130
- (D) OTHER INFORMATION: /standard\_name= "Oligo wps54"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ACACTCTAGA CCACCATGGC TGTCTTGGGG CTGCTCTTCT GCCTGGTGAC ATTCCCAAGC	60
TGTGTCCTAT CCGCTGTCCA GCTGCTAGAG AGTGGTGGCG GTCTGGTGCA GCCAGGAGGA	120
TCTCTGAGAC	130

(2) INFORMATION FOR SEQ ID NO:45:

F1 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: /standard\_name= "Oligo wps57"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ACACTCTAGA AGTTAGGACT CACCTGAAGA GACAGTGACC AGAGTCCCTT GGCCCCAGTA	60
AGCAAAACCG TCGTAATTAT AGTCCCCAGC TCTGGCACAA TAATATATGG CTGTGTCC	118

119

119  
152

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly  
1 5 10 15  
Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Gln Ser Val Ser Thr Ser  
20 25 30  
Thr Tyr Asn Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro  
35 40 45  
Lys Leu Leu Ile Lys Tyr Ala Ser Asn Leu Glu Ser Gly Val Pro Ala  
50 55 60  
Arg Phe Ser Gly Ser Gly Phe Gly Thr Asp Phe Thr Leu Asn Ile His  
65 70 75 80  
Pro Val Glu Glu Glu Asp Thr Val Thr Tyr Tyr Cys Gln His Ser Trp  
85 90 95  
Glu Ile Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys  
100 105 110

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly  
1 5 10 15  
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Thr Ser  
20 25 30

120

120  
153

Thr	Tyr	Asn	Tyr	Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro
		35					40					45			
Arg	Leu	Leu	Ile	Lys	Tyr	Ala	Ser	Asn	Leu	Glu	Ser	Gly	Ile	Pro	Ala
	50					55					60				
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser
65					70					75					80
Arg	Leu	Glu	Ser	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	His	Ser	Trp
				85					90					95	
Glu	Ile	Pro	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Arg	Val	Glu	Ile	Lys	
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Glu	Met	Ile	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Lys	Pro	Gly	Ala
1				5					10					15	
Ser	Leu	Lys	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Asn	Tyr
			20					25					30		
Gly	Leu	Ser	Trp	Val	Arg	Gln	Thr	Ser	Asp	Arg	Arg	Leu	Glu	Trp	Val
		35					40					45			
Ala	Ser	Ile	Ser	Arg	Gly	Gly	Gly	Arg	Ile	Tyr	Ser	Pro	Asp	Asn	Leu
	50					55					60				
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Glu	Asp	Ala	Lys	Asn	Thr	Leu	Tyr
65					70					75					80
Leu	Gln	Met	Ser	Ser	Leu	Lys	Ser	Glu	Asp	Thr	Ala	Leu	Tyr	Tyr	Cys
				85					90					95	
Leu	Arg	Glu	Gly	Ile	Tyr	Tyr	Ala	Asp	Tyr	Gly	Phe	Phe	Asp	Val	Trp
			100					105					110		
Gly	Thr	Gly	Thr	Thr	Val	Ile	Val	Ser	Ser						
		115					120								

121

121  
154

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15  
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr  
20 25 30  
Gly Leu Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45  
Ala Ser Ile Ser Arg Gly Gly Gly Arg Ile Tyr Ser Pro Asp Asn Leu  
50 55 60  
Lys Gly Arg Phe Thr Ile Ser Arg Asn Asp Ser Lys Asn Thr Leu Tyr  
65 70 75 80  
Leu Gln Met Asn Ser Leu Gln Ala Glu Asp Thr Ala Leu Tyr Tyr Cys  
85 90 95  
Leu Arg Glu Gly Ile Tyr Tyr Ala Asp Tyr Gly Phe Phe Asp Val Trp  
100 105 110  
Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
115 120

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

122

122  
155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Asp	Ile	Val	Met	Thr	Gln	Ser	His	Lys	Phe	Met	Ser	Thr	Ser	Val	Gly
1				5					10					15	
Asp	Arg	Val	Ser	Ile	Thr	Cys	Lys	Ala	Ser	Gln	Asp	Val	Gly	Ser	Ala
			20					25					30		
Val	Val	Trp	His	Gln	Gln	Lys	Ser	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile
		35					40					45			
Tyr	Trp	Ala	Ser	Thr	Arg	His	Thr	Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly
		50				55					60				
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Thr	Asn	Val	Gln	Ser
65					70					75					80
Glu	Asp	Leu	Ala	Asp	Tyr	Phe	Cys	Gln	Gln	Tyr	Ser	Ile	Phe	Pro	Leu
				85					90					95	
Thr	Phe	Gly	Ala	Gly	Thr	Arg	Leu	Glu	Leu	Lys					
				100					105						

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Thr	Leu	Ser	Ala	Ser	Val	Gly
1				5					10					15	
Asp	Arg	Val	Thr	Ile	Thr	Cys	Lys	Ala	Ser	Gln	Asp	Val	Gly	Ser	Ala
			20					25					30		
Val	Val	Trp	His	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
		35					40					45			
Tyr	Trp	Ala	Ser	Thr	Arg	His	Thr	Gly	Val	Pro	Ser	Arg	Phe	Thr	Gly
		50				55					60				
Ser	Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65					70					75					80

123

123  
156

Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Tyr Ser Ile Phe Pro Leu  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys  
100 105

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala  
1 5 10 15  
Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Asp His  
20 25 30  
Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Phe  
35 40 45  
Gly Tyr Ile Tyr Pro Arg Asp Gly His Thr Arg Tyr Ser Glu Lys Phe  
50 55 60  
Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ala Ser Thr Ala Tyr  
65 70 75 80  
Met His Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
85 90 95  
Ala Arg Gly Arg Asp Ser Arg Glu Arg Asn Gly Phe Ala Tyr Trp Gly  
100 105 110  
Gln Gly Thr Leu Val Thr Val Ser Ala  
115 120

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

124

124  
137

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser  
1 5 10 15  
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His  
20 25 30  
Thr Ile His Trp Met Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Phe  
35 40 45  
Gly Tyr Ile Tyr Pro Arg Asp Gly His Thr Arg Tyr Ser Glu Lys Phe  
50 55 60  
Lys Gly Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr  
65 70 75 80  
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys  
85 90 95  
Ala Arg Gly Arg Asp Ser Arg Glu Arg Asn Gly Phe Ala Tyr Trp Gly  
100 105 110  
Gln Gly Thr Leu Val Thr Val Ser Ser  
115 120

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly  
1 5 10 15  
Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Asp Asn Tyr  
20 25 30  
Gly Ile Ser Phe Met Asn Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro  
35 40 45

125

125  
158

Lys Leu Leu Ile Tyr Ala Ala Ser Asn Gln Gly Ser Gly Val Pro Ala  
50 55 60  
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Asn Ile His  
65 70 75 80  
Pro Met Glu Glu Asp Asp Thr Ala Met Tyr Phe Cys Gln Gln Ser Lys  
85 90 95  
Glu Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys  
100 105 110

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

F1  
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15  
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Ser Val Asp Asn Tyr  
20 25 30  
Gly Ile Ser Phe Met Asn Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro  
35 40 45  
Lys Leu Leu Ile Tyr Ala Ala Ser Asn Gln Gly Ser Gly Val Pro Ser  
50 55 60  
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser  
65 70 75 80  
Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Lys  
85 90 95  
Glu Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
100 105 110

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

126



126  
159

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala  
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr  
20 25 30

Asn Met His Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile  
35 40 45

Gly Tyr Ile Tyr Pro Tyr Asn Gly Gly Thr Gly Tyr Asn Gln Lys Phe  
50 55 60

Lys Ser Lys Ala Thr Leu Thr Val Asp Asn Ser Ser Ser Thr Ala Tyr  
65 70 75 80

Met Asp Val Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Gly Arg Pro Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val  
100 105 110

Thr Val Ser Ser  
115

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser  
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr  
20 25 30

127

127  
160

Asn	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile
		35					40					45			
Gly	Tyr	Ile	Tyr	Pro	Tyr	Asn	Gly	Gly	Thr	Gly	Tyr	Asn	Gln	Lys	Phe
	50					55					60				
Lys	Ser	Lys	Ala	Thr	Ile	Thr	Ala	Asp	Glu	Ser	Thr	Asn	Thr	Ala	Tyr
65					70					75					80
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85						90					95	
Ala	Arg	Gly	Arg	Pro	Ala	Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val
			100					105					110		
Thr	Val	Ser	Ser												
		115													

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Gln	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Ile	Met	Ser	Ala	Ser	Pro	Gly
1				5					10					15	
Glu	Lys	Val	Thr	Met	Thr	Cys	Ser	Gly	Ser	Ser	Ser	Val	Ser	Phe	Met
			20					25					30		
Tyr	Trp	Tyr	Gln	Gln	Arg	Pro	Gly	Ser	Ser	Pro	Arg	Leu	Leu	Ile	Tyr
		35					40					45			
Asp	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Val	Arg	Phe	Ser	Gly	Ser
		50				55					60				
Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile	Ser	Arg	Met	Glu	Ala	Glu
65					70					75					80
Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp	Ser	Thr	Tyr	Pro	Leu	Thr
				85					90					95	
Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys						
			100					105							

128

128  
161

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15  
Asp Arg Val Thr Ile Thr Cys Ser Gly Ser Ser Ser Val Ser Phe Met  
20 25 30  
Tyr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr  
35 40 45  
Asp Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser  
50 55 60  
Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu  
65 70 75 80  
F) Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Thr Tyr Pro Leu Thr  
85 90 95  
Phe Gly Gln Gly Thr Lys Val Glu Val Lys  
100 105

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln  
1 5 10 15

129

129  
162

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Val Thr Ser Tyr  
20 25 30  
Gly Val His Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu  
35 40 45  
Gly Val Ile Trp Ser Gly Gly Ser Thr Asp Tyr Asn Ala Ala Phe Ile  
50 55 60  
Ser Arg Leu Thr Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Phe  
65 70 75 80  
Lys Val Asn Ser Leu Gln Pro Ala Asp Thr Ala Ile Tyr Tyr Cys Ala  
85 90 95  
Arg Ala Gly Asp Tyr Asn Tyr Asp Gly Phe Ala Tyr Trp Gly Gln Gly  
100 105 110  
Thr Leu Val Thr Val Ser Ala  
115

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15  
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Val Thr Ser Tyr  
20 25 30  
Gly Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45  
Gly Val Ile Trp Ser Gly Gly Ser Thr Asp Tyr Asn Ala Ala Phe Ile  
50 55 60  
Ser Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu  
65 70 75 80  
Gln Met Asn Ser Leu Gln Ala Glu Asp Thr Ala Ile Tyr Tyr Cys Ala  
85 90 95

130

130  
163

Arg Ala Gly Asp Tyr Asn Tyr Asp Gly Phe Ala Tyr Trp Gly Gln Gly  
100 105 110

Thr Leu Val Thr Val Ser Ser  
115

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Thr Pro Gly  
1 5 10 15

Asp Ser Val Ser Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Asn Asn  
20 25 30

Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile  
35 40 45

Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly  
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Val Asn Gly Val Glu Thr  
65 70 75 80

Glu Asp Phe Gly Met Tyr Phe Cys Gln Gln Ser Asn Ser Trp Pro His  
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys  
100 105

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

131

131  
164

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser	Leu	Ser	Pro	Gly
1				5					10					15	
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Ser	Asn	Asn
			20					25					30		
Leu	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile
			35				40					45			
Lys	Tyr	Ala	Ser	Gln	Ser	Ile	Ser	Gly	Ile	Pro	Asp	Arg	Phe	Ser	Gly
	50					55					60				
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu	Pro
65					70					75				80	
Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Ser	Asn	Ser	Trp	Pro	His
				85					90					95	
Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys					
			100					105							

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Glu	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Val	Lys	Pro	Gly	Ala
1				5					10					15	
Ser	Met	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Val	Tyr	Ser	Phe	Thr	Gly	Tyr
			20					25					30		
Thr	Met	Asn	Trp	Val	Lys	Gln	Ser	His	Gly	Gln	Asn	Leu	Glu	Trp	Ile
			35				40					45			
Gly	Leu	Ile	Asn	Pro	Tyr	Asn	Gly	Gly	Thr	Ser	Tyr	Asn	Gln	Lys	Phe
	50					55					60				
Lys	Gly	Lys	Ala	Thr	Leu	Thr	Val	Asp	Lys	Ser	Ser	Asn	Thr	Ala	Tyr
65					70					75				80	

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Met Glu Leu Leu Ser Leu Thr Ser Ala Asp Ser Ala Val Tyr Tyr Cys  
85 90 95  
Thr Arg Arg Gly Phe Arg Asp Tyr Ser Met Asp Tyr Trp Gly Gln Gly  
100 105 110  
Thr Ser Val Thr Val Ser Ser  
115

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser  
1 5 10 15  
Ser Val Arg Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr  
20 25 30  
Thr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45  
Gly Leu Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe  
50 55 60  
Lys Gly Arg Val Thr Val Ser Leu Lys Pro Ser Phe Asn Gln Ala Tyr  
65 70 75 80  
Met Glu Leu Ser Ser Leu Phe Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95  
Thr Arg Arg Gly Phe Arg Asp Tyr Ser Met Asp Tyr Trp Gly Gln Gly  
100 105 110  
Thr Leu Val Thr Val Ser Ser  
115

F1

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166

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 393 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ATG	GAG	AAA	GAC	ACA	CTC	CTG	CTA	TGG	GTC	CTG	CTT	CTC	TGG	GTT	CCA	48
Met	Glu	Lys	Asp	Thr	Leu	Leu	Leu	Trp	Val	Leu	Leu	Leu	Trp	Val	Pro	
1				5				10					15			
GGT	TCC	ACA	GGT	GAC	ATT	GTG	CTG	ACC	CAA	TCT	CCA	GCT	TCT	TTG	GCT	96
Gly	Ser	Thr	Gly	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Ser	Leu	Ala	
			20					25					30			
GTG	TCT	CTA	GGG	CAG	AGG	GCC	ACC	ATC	TCC	TGC	AGA	GCC	AGC	GAA	AGT	144
Val	Ser	Leu	Gly	Gln	Arg	Ala	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Glu	Ser	
			35				40					45				
GTT	GAT	AAT	TAT	GGC	ATT	AGT	TTT	ATG	AAC	TGG	TTC	CAA	CAG	AAA	CCA	192
Val	Asp	Asn	Tyr	Gly	Ile	Ser	Phe	Met	Asn	Trp	Phe	Gln	Gln	Lys	Pro	
	50					55					60					
GGA	CAG	CCA	CCC	AAA	CTC	CTC	ATC	TAT	GCT	GCA	TCC	AAC	CAA	GGA	TCC	240
Gly	Gln	Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Ala	Ala	Ser	Asn	Gln	Gly	Ser	
65					70				75					80		
GGG	GTC	CCT	GCC	AGG	TTT	AGT	GGC	AGT	GGG	TCT	GGG	ACA	GAC	TTC	AGC	288
Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Ser	
				85				90					95			
CTC	AAC	ATC	CAT	CCT	ATG	GAG	GAG	GAT	GAT	ACT	GCA	ATG	TAT	TTC	TGT	336
Leu	Asn	Ile	His	Pro	Met	Glu	Glu	Asp	Asp	Thr	Ala	Met	Tyr	Phe	Cys	
			100					105					110			
CAG	CAA	AGT	AAG	GAG	GTT	CCG	TGG	ACG	TTC	GGT	GGA	GGC	ACC	AAG	CTG	384
Gln	Gln	Ser	Lys	Glu	Val	Pro	Trp	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	
			115				120					125				
GAA	ATC	AAA														393
Glu	Ile	Lys														
130																

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(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 131 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Met Glu Lys Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro  
1 5 10 15  
Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala  
20 25 30  
Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser  
35 40 45  
Val Asp Asn Tyr Gly Ile Ser Phe Met Asn Trp Phe Gln Gln Lys Pro  
50 55 60  
Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Gln Gly Ser  
65 70 75 80  
Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ser  
85 90 95  
Leu Asn Ile His Pro Met Glu Glu Asp Asp Thr Ala Met Tyr Phe Cys  
100 105 110  
Gln Gln Ser Lys Glu Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu  
115 120 125  
Glu Ile Lys  
130

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 405 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 1..405

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

ATG	GGA	TGG	AGC	TGG	ATC	TTT	CTC	TTC	CTC	CTG	TCA	GGA	ACT	GCA	GGC	48
Met	Gly	Trp	Ser	Trp	Ile	Phe	Leu	Phe	Leu	Leu	Ser	Gly	Thr	Ala	Gly	
1				5					10					15		
GTC	CAC	TCT	GAG	GTC	CAG	CTT	CAG	CAG	TCA	GGA	CCT	GAG	CTG	GTG	AAA	96
Val	His	Ser	Glu	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Val	Lys	
			20					25					30			
CCT	GGG	GCC	TCA	GTG	AAG	ATA	TCC	TGC	AAG	GCT	TCT	GGA	TAC	ACA	TTC	144
Pro	Gly	Ala	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	
		35					40					45				
ACT	GAC	TAC	AAC	ATG	CAC	TGG	GTG	AAG	CAG	AGC	CAT	GGA	AAG	AGC	CTT	192
Thr	Asp	Tyr	Asn	Met	His	Trp	Val	Lys	Gln	Ser	His	Gly	Lys	Ser	Leu	
	50					55					60					
GAG	TGG	ATT	GGA	TAT	ATT	TAT	CCT	TAC	AAT	GGT	GGT	ACT	GGC	TAC	AAC	240
Glu	Trp	Ile	Gly	Tyr	Ile	Tyr	Pro	Tyr	Asn	Gly	Gly	Thr	Gly	Tyr	Asn	
65					70				75						80	
CAG	AAG	TTC	AAG	AGC	AAG	GCC	ACA	TTG	ACT	GTA	GAC	AAT	TCC	TCC	AGC	288
Gln	Lys	Phe	Lys	Ser	Lys	Ala	Thr	Leu	Thr	Val	Asp	Asn	Ser	Ser	Ser	
				85				90						95		
ACA	GCC	TAC	ATG	GAC	GTC	CGC	AGC	CTG	ACA	TCT	GAG	GAC	TCT	GCA	GTC	336
Thr	Ala	Tyr	Met	Asp	Val	Arg	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	
			100					105						110		
TAT	TAC	TGT	GCA	AGA	GGG	CGC	CCC	GCT	ATG	GAC	TAC	TGG	GGT	CAA	GGA	384
Tyr	Tyr	Cys	Ala	Arg	Gly	Arg	Pro	Ala	Met	Asp	Tyr	Trp	Gly	Gln	Gly	
		115					120					125				
ACC	TCA	GTC	ACC	GTC	TCC	TCA										405
Thr	Ser	Val	Thr	Val	Ser	Ser										
	130					135										

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 135 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met	Gly	Trp	Ser	Trp	Ile	Phe	Leu	Phe	Leu	Leu	Ser	Gly	Thr	Ala	Gly
1				5					10					15	

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Val His Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys  
20 25 30

Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
35 40 45

Thr Asp Tyr Asn Met His Trp Val Lys Gln Ser His Gly Lys Ser Leu  
50 55 60

Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Gly Gly Thr Gly Tyr Asn  
65 70 75 80

Gln Lys Phe Lys Ser Lys Ala Thr Leu Thr Val Asp Asn Ser Ser Ser  
85 90 95

Thr Ala Tyr Met Asp Val Arg Ser Leu Thr Ser Glu Asp Ser Ala Val  
100 105 110

Tyr Tyr Cys Ala Arg Gly Arg Pro Ala Met Asp Tyr Trp Gly Gln Gly  
115 120 125

Thr Ser Val Thr Val Ser Ser  
130 135

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 107 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly  
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asn Thr Trp  
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Met  
35 40 45

Tyr Lys Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ile Gly  
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80

137

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Asp	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Tyr	Asn	Ser	Asp	Ser	Lys
				85					90					95	
Met	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Val	Lys					
			100					105							

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 111 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5					10					15	
Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Glu	Ser	Val	Asp	Asn	Tyr
			20					25					30		
Gly	Ile	Ser	Phe	Met	Asn	Trp	Phe	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro
		35					40					45			
Lys	Leu	Leu	Ile	Tyr	Ala	Ala	Ser	Asn	Gln	Gly	Ser	Gly	Val	Pro	Ser
	50					55					60				
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser
65					70					75				80	
Ser	Leu	Gln	Pro	Asp	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Lys
				85					90					95	
Glu	Val	Pro	Trp	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 117 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

[illegible]

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ser
1			5						10					15	
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asp	Tyr
			20					25					30		
Asn	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile
		35					40					45			
Gly	Tyr	Ile	Tyr	Pro	Tyr	Asn	Gly	Gly	Thr	Gly	Tyr	Asn	Gln	Lys	Phe
	50					55					60				

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Lys Ser Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr  
65 70 75 80  
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95  
Ala Arg Gly Arg Pro Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val  
100 105 110  
Thr Val Ser Ser  
115

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (oligonucleotide)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

TATATCTAGA CCACCATGGG ATGGAGCTGG ATCTTTCTCT TCCTCCTGTC AGGAACTGCT 60  
GGCGTCCACT CTCAGGTTCA GCTGGTGCAG TCTGGAGCTG AGGTGAAGAA GCCTGGGAGC 120  
TCAGTGAAGG TT 132

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (oligonucleotide)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

AGCCGGTACC ACCATTGTAA GGATAAATAT ATCCAATCCA TTCCAGGCCT TGGCCAGGAG 60  
CCTGCCTCAC CCAGTGCATG TTGTAGTCAG TGAAGGTGTA GCCAGAAGCT TTGCAGGAAA 120  
CCTTCACTGA GCT 133

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(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (oligonucleotide)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

TGGTGGTACC GGCTACAACC AGAAGTTCAA GAGCAAGGCC ACAATTACAG CAGACGAGAG	60
TACTAACACA GCCTACATGG AACTCTCCAG CCTGAGGTCT GAGGACACTG CA	112

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (oligonucleotide)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

TATATCTAGA GGCCATTCTT ACCTGAAGAG ACAGTGACCA GAGTCCCTTG GCCCCAGTAG	60
TCCATAGCGG GCGGCCCTCT TCGGCAGTAA TAGACTGCAG TGTCCTCAGA C	111

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (oligonucleotide)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

TATATCTAGA CCACCATGGA GAAAGACACA CTCCTGCTAT GGGTCCTGCT TCTCTGGGTT	60
CCAGGTTCCA CAGGTGACAT TCAGATGACC CAGTCTCCGA GCTCTCTGTC CGCATCAGTA	120
GG	122

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (oligonucleotide)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

TCAGAAGCTT AGGAGCCTTC CCGGGTTTCT GTTGGAACCA GTTCATAAAG CTAATGCCAT	60
AATTGTCGAC ACTTTCGCTG GCTCTGCATG TGATGGTGAC CCTGTCTCCT ACTGATGCGG	120
AC	122

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (oligonucleotide)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TCCTAAGCTT CTGATTTACG CTGCATCCAA CCAAGGCTCC GGGGTACCCT CTCGCTTCTC	60
AGGCAGTGGG TCTGGGACAG ACTTCACTCT CACCATTTCG TCTCTGCAGC CTGATGACT	119

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

TATATCTAGA CCACCATGGA GAAAGACACA CTCCTGCTAT GGGTCCTGCT TCTCTGGGTT	60
CCAGGTTC CA CAGGTGACAT TCAGATGACC CAGTCTCCGA GCTCTCTGTC CGCATCAGTA	120
GG	122

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (oligonucleotide)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

TCAGAAGCTT AGGAGCCTTC CCGGGTTTCT GTTGAACCA GTTCATAAAG CTAATGCCAT	60
AATTGTCGAC ACTTTCGCTG GCTCTGCATG TGATGGTGAC CCTGTCTCCT ACTGATGCGG	120
AC	122

F1

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (oligonucleotide)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TCCTAAGCTT CTGATTTACG CTGCATCCAA CCAAGGCTCC GGGGTACCCT CTCGCTTCTC	60
AGGCAGTGG A TCTGGGACAG ACTTCACTCT CACCATTTC A TCTCTGCAGC CTGATGACT	119

143

143  
175

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (oligonucleotide)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TATATCTAGA CTTTGGATTC TACTTACGTT TGATCTCCAC CTTGGTCCCT TGACCGAACG	60
TCCACGGAAC CTCCTTACTT TGCTGACAGT AATAGGTTGC GAAGTCATCA GGCTGCAG	118

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

F1

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

ATG GTT TTC ACA CCT CAG ATA CTT GGA CTT ATG CTT TTT TGG ATT TCA	48
Met Val Phe Thr Pro Gln Ile Leu Gly Leu Met Leu Phe Trp Ile Ser	
1 5 10 15	
GCC TCC AGA GGT GAT ATT GTG CTA ACT CAG TCT CCA GCC ACC CTG TCT	96
Ala Ser Arg Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser	
20 25 30	
GTG ACT CCG GGA GAT AGC GTC AGT CTT TCC TGC AGG GCC AGC CAA AGT	144
Val Thr Pro Gly Asp Ser Val Ser Leu Ser Cys Arg Ala Ser Gln Ser	
35 40 45	
ATT AGC AAC AAC CTA CAC TGG TAT CAA CAA AAA TCA CAT GAG TCT CCA	192
Ile Ser Asn Asn Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro	
50 55 60	

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AGG	CTT	CTC	ATC	AAG	TAT	GCT	TCC	CAG	TCC	ATC	TCT	GGG	ATC	CCC	TCC	240
Arg	Leu	Leu	Ile	Lys	Tyr	Ala	Ser	Gln	Ser	Ile	Ser	Gly	Ile	Pro	Ser	
65					70					75					80	
AGG	TTC	AGT	GGC	AGT	GGA	TCA	GGG	ACA	GAT	TTC	ACT	CTC	AGT	GTC	AAC	288
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Ser	Val	Asn	
				85					90					95		
GGT	GTG	GAG	ACT	GAA	GAT	TTT	GGA	ATG	TAT	TTC	TGT	CAA	CAG	AGT	AAC	336
Gly	Val	Glu	Thr	Glu	Asp	Phe	Gly	Met	Tyr	Phe	Cys	Gln	Gln	Ser	Asn	
			100					105						110		
AGT	TGG	CCT	CAT	ACG	TTC	GGA	GGG	GGG	ACC	AAG	CTG	GAA	ATA	AAA		381
Ser	Trp	Pro	His	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys		
		115						120					125			

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 127 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Met	Val	Phe	Thr	Pro	Gln	Ile	Leu	Gly	Leu	Met	Leu	Phe	Trp	Ile	Ser	
1				5					10					15		
Ala	Ser	Arg	Gly	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	
			20					25					30			
Val	Thr	Pro	Gly	Asp	Ser	Val	Ser	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	
		35					40					45				
Ile	Ser	Asn	Asn	Leu	His	Trp	Tyr	Gln	Gln	Lys	Ser	His	Glu	Ser	Pro	
	50					55					60					
Arg	Leu	Leu	Ile	Lys	Tyr	Ala	Ser	Gln	Ser	Ile	Ser	Gly	Ile	Pro	Ser	
65					70					75					80	
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Ser	Val	Asn	
				85					90					95		
Gly	Val	Glu	Thr	Glu	Asp	Phe	Gly	Met	Tyr	Phe	Cys	Gln	Gln	Ser	Asn	
			100					105						110		
Ser	Trp	Pro	His	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys		
		115						120					125			

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(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..414

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

ATG	GGA	TGG	AGC	TGG	ATC	TTT	CTC	TTC	CTC	CTG	TCA	GGA	ACT	GCA	GGT	48
Met	Gly	Trp	Ser	Trp	Ile	Phe	Leu	Phe	Leu	Leu	Ser	Gly	Thr	Ala	Gly	
1				5					10					15		
GTC	CAC	TCT	GAG	GTC	CAG	CTG	CAA	CAG	TCT	GGA	CCT	GAG	CTG	GTG	AAG	96
Val	His	Ser	Glu	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Val	Lys	
			20					25					30			
CCT	GGA	GCT	TCA	ATG	AAG	ATA	TCC	TGC	AAG	GCT	TCT	GTT	TAC	TCA	TTC	144
Pro	Gly	Ala	Ser	Met	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Val	Tyr	Ser	Phe	
		35					40					45				
ACT	GGC	TAC	ACC	ATG	AAC	TGG	GTG	AAG	CAG	AGC	CAT	GGA	CAG	AAC	CTT	192
Thr	Gly	Tyr	Thr	Met	Asn	Trp	Val	Lys	Gln	Ser	His	Gly	Gln	Asn	Leu	
	50					55				60						
GAG	TGG	ATT	GGA	CTT	ATT	AAT	CCT	TAC	AAT	GGT	GGT	ACT	AGC	TAC	AAC	240
Glu	Trp	Ile	Gly	Leu	Ile	Asn	Pro	Tyr	Asn	Gly	Gly	Thr	Ser	Tyr	Asn	
65				70					75						80	
CAG	AAG	TTC	AAG	GGG	AAG	GCC	ACA	TTA	ACT	GTA	GAC	AAG	TCA	TCC	AAC	288
Gln	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Val	Asp	Lys	Ser	Ser	Asn	
			85					90						95		
ACA	GCC	TAC	ATG	GAG	CTC	CTC	AGT	CTG	ACA	TCT	GCG	GAC	TCT	GCA	GTC	336
Thr	Ala	Tyr	Met	Glu	Leu	Leu	Ser	Leu	Thr	Ser	Ala	Asp	Ser	Ala	Val	
			100					105					110			
TAT	TAC	TGT	ACA	AGA	CGG	GGG	TTT	CGA	GAC	TAT	TCT	ATG	GAC	TAC	TGG	384
Tyr	Tyr	Cys	Thr	Arg	Arg	Gly	Phe	Arg	Asp	Tyr	Ser	Met	Asp	Tyr	Trp	
		115				120						125				
GGT	CAA	GGA	ACC	TCA	GTC	ACC	GTC	TCC	TCA							414
Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser							
	130					135										

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(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly  
1 5 10 15  
Val His Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys  
20 25 30  
Pro Gly Ala Ser Met Lys Ile Ser Cys Lys Ala Ser Val Tyr Ser Phe  
35 40 45  
Thr Gly Tyr Thr Met Asn Trp Val Lys Gln Ser His Gly Gln Asn Leu  
50 55 60  
Glu Trp Ile Gly Leu Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn  
65 70 75 80  
Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Asn  
85 90 95  
F1 Thr Ala Tyr Met Glu Leu Leu Ser Leu Thr Ser Ala Asp Ser Ala Val  
100 105 110  
Tyr Tyr Cys Thr Arg Arg Gly Phe Arg Asp Tyr Ser Met Asp Tyr Trp  
115 120 125  
Gly Gln Gly Thr Ser Val Thr Val Ser Ser  
130 135

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly  
1 5 10 15

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Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Gly
			20					25					30		
Tyr	Leu	Gly	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu
		35					40					45			
Ile	Tyr	Gly	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Ile	Pro	Asp	Arg	Phe	Ser
	50					55					60				
Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu
65					70					75					80
Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	Gly	Ser	Leu	Gly
				85					90					95	
Arg	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys				
			100					105							

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser	Leu	Ser	Pro	Gly
1				5					10					15	
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Ser	Asn	Asn
			20					25					30		
Leu	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile
		35				40						45			
Lys	Tyr	Ala	Ser	Gln	Ser	Ile	Ser	Gly	Ile	Pro	Asp	Arg	Phe	Ser	Gly
	50					55					60				
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu	Pro
65				70						75				80	
Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Ser	Asn	Ser	Trp	Pro	His
				85				90						95	
Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys					
			100					105							

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(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Gln Val Gln Leu Met Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser  
1 5 10 15  
Ser Val Arg Val Ser Cys Lys Thr Ser Gly Gly Thr Phe Val Asp Tyr  
20 25 30  
Lys Gly Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45  
Gly Gln Ile Pro Leu Arg Phe Asn Gly Glu Val Lys Asn Pro Gly Ser  
50 55 60  
Val Val Arg Val Ser Val Ser Leu Lys Pro Ser Phe Asn Gln Ala His  
65 70 75 80  
Met Glu Leu Ser Ser Leu Phe Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95  
Ala Arg Glu Tyr Gly Phe Asp Thr Ser Asp Tyr Tyr Tyr Tyr Tyr Trp  
100 105 110  
Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
115 120

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser  
1 5 10 15

149

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Ser	Val	Arg	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ser	Phe	Thr	Gly	Tyr
			20					25					30		
Thr	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			
Gly	Leu	Ile	Asn	Pro	Tyr	Asn	Gly	Gly	Thr	Ser	Tyr	Asn	Gln	Lys	Phe
	50					55					60				
Lys	Gly	Arg	Val	Thr	Val	Ser	Leu	Lys	Pro	Ser	Phe	Asn	Gln	Ala	Tyr
65					70					75					80
Met	Glu	Leu	Ser	Ser	Leu	Phe	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Thr	Arg	Arg	Gly	Phe	Arg	Asp	Tyr	Ser	Met	Asp	Tyr	Trp	Gly	Gln	Gly
			100					105					110		
Thr	Leu	Val	Thr	Val	Ser	Ser									

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (oligonucleotide)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

TAGATCTAGA CCACCATGGT TTTCACACCT CAGATACTCA GACTCATGCT CTTCTGGATT	60
TCAGCCTCCA GAGGTGAAAT TGTGCTAACT CAGTCTCCAG GCACCCTAAG CTTATCACCG	120
GGAGAAAGG	129

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (oligonucleotide)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TAGACAGAAT TCACGCGTAC TTGATAAGTA GACGTGGAGC TTGTCCAGGT TTTTGTGTTGGT	60
ACCAGTGTAG GTTGTGCTA ATACTTTGGC TGGCCCTGCA GGAAAGTGTA GCCCTTTCTC	120
CCGGTGAT	128

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (oligonucleotide)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

AAGAGAATTC ACGCGTCCCA GTCCATCTCT GGAATACCCG ATAGGTTTCAG TGGCAGTGGA	60
TCAGGGACAG ATTTCACTCT CACAATAAGT AGGCTCGAGC CGGAAGATTT TGC	113

F1

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (oligonucleotide)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

TAGATCTAGA GTTGAGAAGA CTACTIONAGT TTTATTTCTA CCTTGGTCCC TTGTCCGAAC	60
GTATGAGGCC AACTGTTACT CTGTTGACAA TAATACACAG CAAAATCTTC CGGCTC	116

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(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (oligonucleotide)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

TATATCTAGA CCACCATGGG ATGGAGCTGG ATCTTTCTCT TCCTCCTGTC AGGAACTGCA	60
GGTGTCCACT CTCAAGTCCA ACTGGTACAG TCTGGAGCTG AGGTTAAAAA GCCTGGAAGT	120
TCAGTAAGAG TTTC	134

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

F (ii) MOLECULE TYPE: DNA (oligonucleotide)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

TATATAGGTA CCACCATGGG ATGGAGCTGG ATCTTTCTCT TCCTCCTGTC AGGAACTGCA	60
TGCCTGTCTC ACCCAGTTCA TGGTATACCC AGTGAATGAG TATCCGGAAG CTTTGCAGGA	120
AACTCTTACT GAAC	134

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (oligonucleotide)

152

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

TATATAGGTA CCAGCTACAA CCAGAAGTTC AAGGGCAGAG TTACAGTTTC TTTGAAGCCT 60  
TCATTTAACC AGGCCTACAT GGAGCTCAGT AGTCTGTTTT CTGAAGACAC TGCAGT 116

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (oligonucleotide)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

TATATCTAGA GGCCATTCTT ACCTGAGGAG ACGGTGACTA AGGTTTCCTTG ACCCCAGTAG 60  
TCCATAGAAT AGTCTCGAAA CCCCCGTCTT GTACAGTAAT AGACTGCAGT GTCTTC 116

F1  
(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

ATG CAT CAG ACC AGC ATG GGC ATC AAG ATG GAA TCA CAG ACT CTG GTC 48  
Met His Gln Thr Ser Met Gly Ile Lys Met Glu Ser Gln Thr Leu Val  
1 5 10 15

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TTC	ATA	TCC	ATA	CTG	CTC	TGG	TTA	TAT	GGT	GCT	GAT	GGG	AAC	ATT	GTT	96
Phe	Ile	Ser	Ile	Leu	Leu	Trp	Leu	Tyr	Gly	Ala	Asp	Gly	Asn	Ile	Val	
			20					25					30			
ATG	ACC	CAA	TCT	CCC	AAA	TCC	ATG	TAC	GTG	TCA	ATA	GGA	GAG	AGG	GTC	144
Met	Thr	Gln	Ser	Pro	Lys	Ser	Met	Tyr	Val	Ser	Ile	Gly	Glu	Arg	Val	
		35					40					45				
ACC	TTG	AGC	TGC	AAG	GCC	AGT	GAA	AAT	GTG	GAT	ACT	TAT	GTA	TCC	TGG	192
Thr	Leu	Ser	Cys	Lys	Ala	Ser	Glu	Asn	Val	Asp	Thr	Tyr	Val	Ser	Trp	
	50					55					60					
TAT	CAA	CAG	AAA	CCA	GAG	CAG	TCT	CCT	AAA	CTG	CTG	ATA	TAT	GGG	GCA	240
Tyr	Gln	Gln	Lys	Pro	Glu	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Gly	Ala	
65					70					75					80	
TCC	AAC	CGG	TAC	ACT	GGG	GTC	CCC	GAT	CGC	TTC	ACG	GGC	AGT	GGA	TCT	288
Ser	Asn	Arg	Tyr	Thr	Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly	Ser	Gly	Ser	
				85					90					95		
GCA	ACA	GAT	TTC	ACT	CTG	ACC	ATC	AGC	AGT	GTG	CAG	GCT	GAA	GAC	CTT	336
Ala	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Val	Gln	Ala	Glu	Asp	Leu	
			100					105					110			
GCA	GAT	TAT	CAC	TGT	GGA	CAG	AGT	TAC	AAC	TAT	CCA	TTC	ACG	TTC	GGC	384
Ala	Asp	Tyr	His	Cys	Gly	Gln	Ser	Tyr	Asn	Tyr	Pro	Phe	Thr	Phe	Gly	
		115					120					125				
TCG	GGG	ACA	AAG	TTG	GAA	ATA	AAG									408
Ser	Gly	Thr	Lys	Leu	Glu	Ile	Lys									
	130					135										

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Met	His	Gln	Thr	Ser	Met	Gly	Ile	Lys	Met	Glu	Ser	Gln	Thr	Leu	Val
1				5					10					15	
Phe	Ile	Ser	Ile	Leu	Leu	Trp	Leu	Tyr	Gly	Ala	Asp	Gly	Asn	Ile	Val
			20					25					30		
Met	Thr	Gln	Ser	Pro	Lys	Ser	Met	Tyr	Val	Ser	Ile	Gly	Glu	Arg	Val
		35					40					45			

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Thr	Leu	Ser	Cys	Lys	Ala	Ser	Glu	Asn	Val	Asp	Thr	Tyr	Val	Ser	Trp
50						55					60				
Tyr	Gln	Gln	Lys	Pro	Glu	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Gly	Ala
65					70					75					80
Ser	Asn	Arg	Tyr	Thr	Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly	Ser	Gly	Ser
				85					90					95	
Ala	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Val	Gln	Ala	Glu	Asp	Leu
			100					105					110		
Ala	Asp	Tyr	His	Cys	Gly	Gln	Ser	Tyr	Asn	Tyr	Pro	Phe	Thr	Phe	Gly
		115					120					125			
Ser	Gly	Thr	Lys	Leu	Glu	Ile	Lys								
130						135									

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 456 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

ATG	ACA	TCA	CTG	TTC	TCT	CTA	CAG	TTA	CCG	AGC	ACA	CAG	GAC	CTC	GCC	48
Met	Thr	Ser	Leu	Phe	Ser	Leu	Gln	Leu	Pro	Ser	Thr	Gln	Asp	Leu	Ala	
1				5				10					15			
ATG	GGA	TGG	AGC	TGT	ATC	ATC	CTC	TTC	TTG	GTA	GCA	ACA	GCT	ACA	GGT	96
Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly	
			20				25						30			
GTC	CTC	TCC	CAG	GTC	CAA	CTG	CAG	CAG	CCT	GGG	GCT	GAC	CTT	GTG	ATG	144
Val	Leu	Ser	Gln	Val	Gln	Leu	Gln	Gln	Pro	Gly	Ala	Asp	Leu	Val	Met	
			35				40					45				
CCT	GGG	GCT	CCA	GTG	AAG	CTG	TCC	TGC	TTG	GCT	TCT	GGC	TAC	ATC	TTC	192
Pro	Gly	Ala	Pro	Val	Lys	Leu	Ser	Cys	Leu	Ala	Ser	Gly	Tyr	Ile	Phe	
50						55					60					

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ACC	AGC	TCC	TGG	ATA	AAC	TGG	GTG	AAG	CAG	AGG	CCT	GGA	CGA	GGC	CTC	240
Thr	Ser	Ser	Trp	Ile	Asn	Trp	Val	Lys	Gln	Arg	Pro	Gly	Arg	Gly	Leu	
65					70					75					80	
GAG	TGG	ATT	GGA	AGG	ATT	GAT	CCT	TCC	GAT	GGT	GAA	GTT	CAC	TAC	AAT	288
Glu	Trp	Ile	Gly	Arg	Ile	Asp	Pro	Ser	Asp	Gly	Glu	Val	His	Tyr	Asn	
				85					90					95		
CAA	GAT	TTC	AAG	GAC	AAG	GCC	ACA	CTG	ACT	GTA	GAC	AAA	TCC	TCC	AGC	336
Gln	Asp	Phe	Lys	Asp	Lys	Ala	Thr	Leu	Thr	Val	Asp	Lys	Ser	Ser	Ser	
			100					105					110			
ACA	GCC	TAC	ATC	CAA	CTC	AAC	AGC	CTG	ACA	TCT	GAG	GAC	TCT	GCG	GTC	384
Thr	Ala	Tyr	Ile	Gln	Leu	Asn	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	
		115					120					125				
TAT	TAC	TGT	GCT	AGA	GGA	TTT	CTG	CCC	TGG	TTT	GCT	GAC	TGG	GGC	CAA	432
Tyr	Tyr	Cys	Ala	Arg	Gly	Phe	Leu	Pro	Trp	Phe	Ala	Asp	Trp	Gly	Gln	
	130					135					140					
GGG	ACT	CTG	GTC	ACT	GTC	TCT	GCA									456
Gly	Thr	Leu	Val	Thr	Val	Ser	Ala									
145					150											

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Met	Thr	Ser	Leu	Phe	Ser	Leu	Gln	Leu	Pro	Ser	Thr	Gln	Asp	Leu	Ala
1				5					10					15	
Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly
			20					25					30		
Val	Leu	Ser	Gln	Val	Gln	Leu	Gln	Gln	Pro	Gly	Ala	Asp	Leu	Val	Met
		35					40					45			
Pro	Gly	Ala	Pro	Val	Lys	Leu	Ser	Cys	Leu	Ala	Ser	Gly	Tyr	Ile	Phe
	50					55					60				
Thr	Ser	Ser	Trp	Ile	Asn	Trp	Val	Lys	Gln	Arg	Pro	Gly	Arg	Gly	Leu
65					70					75					80
Glu	Trp	Ile	Gly	Arg	Ile	Asp	Pro	Ser	Asp	Gly	Glu	Val	His	Tyr	Asn
				85					90					95	

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Gln	Asp	Phe	Lys	Asp	Lys	Ala	Thr	Leu	Thr	Val	Asp	Lys	Ser	Ser	Ser
			100					105					110		
Thr	Ala	Tyr	Ile	Gln	Leu	Asn	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val
		115					120					125			
Tyr	Tyr	Cys	Ala	Arg	Gly	Phe	Leu	Pro	Trp	Phe	Ala	Asp	Trp	Gly	Gln
	130					135					140				
Gly	Thr	Leu	Val	Thr	Val	Ser	Ala								
145					150										

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Thr	Leu	Ser	Ala	Ser	Val	Gly
1				5					10					15	
Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Asn	Thr	Trp
		20						25					30		
Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Met
		35				40						45			
Tyr	Lys	Ala	Ser	Ser	Leu	Glu	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ile	Gly
	50					55					60				
Ser	Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
	65				70					75					80
Asp	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Tyr	Asn	Ser	Asp	Ser	Lys
				85					90					95	
Met	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Val	Lys					
			100					105							

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(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 107 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly  
 1 5 10 15  
 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Glu Asn Val Asp Thr Tyr  
 20 25 30  
 Val Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45  
 Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60  
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
 65 70 75 80  
 Asp Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Ser Tyr Asn Tyr Pro Phe  
 85 90 95  
 Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys  
 100 105

F1

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 117 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser  
 1 5 10 15

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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Arg Ser  
20 25 30  
Ala Ile Ile Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
35 40 45  
Gly Gly Ile Val Pro Met Phe Gly Pro Pro Asn Tyr Ala Gln Lys Phe  
50 55 60  
Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr  
65 70 75 80  
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe Tyr Phe Cys  
85 90 95  
Ala Gly Gly Tyr Gly Ile Tyr Ser Pro Glu Glu Tyr Asn Gly Gly Leu  
100 105 110  
Val Thr Val Ser Ser  
115

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser  
1 5 10 15  
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Ser Ser  
20 25 30  
Trp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
35 40 45  
Gly Arg Ile Asp Pro Ser Asp Gly Glu Val His Tyr Asn Gln Asp Phe  
50 55 60  
Lys Asp Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr  
65 70 75 80  
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

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Ala Arg Gly Phe Leu Pro Trp Phe Ala Asp Trp Gly Gln Gly Thr Leu  
100 105 110  
Val Thr Val Ser Ser  
115

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (oligonucleotide)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

TTTTTTCTAG ACCACCATGG AGACCGATAC CCTCCTGCTA TGGGTCCTCC TGCTATGGGT	60
CCCAGGATCA ACCGGAGATA TTCAGATGAC CCAGTCTCCG TCGACCCTCT CTGCT	115

(2) INFORMATION FOR SEQ ID NO:107:

F<sub>1</sub> (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (oligonucleotide)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

TTTTAAGCTT GGGAGCTTTG CCTGGCTTCT GCTGATACCA GGATACATAA GTATCCACAT	60
TTTCACTGGC CTTGCAGGTT ATGGTGACCC TATCCCCGAC GCTAGCAGAG AGGGTCGACG	120

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs

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192

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (oligonucleotide)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

TTTTAAGCTT CTAATTTATG GGGCATCCAA CCGGTACACT GGGGTACCTT CACGCTTCAG	60
TGGCAGTGGA TCTGGGACCG ATTTACCCT CACAATCAGC TCTCTGCAGC CAGATGAT	118

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (oligonucleotide)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

TTTTTTCTAG AGCAAAGTC TACTTACGTT TGACCTCCAC CTTGGTCCCC TGACCGAACG	60
TGAATGGATA GTTGTAAGTC TGTCCGCACT AATAAGTGGC GAAATCATCT GGCTGCAGAG	120

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (oligonucleotide)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

TTTTTCTAGA CCACCATGGG ATGGAGCTGG ATCTTTCTCT TCCTCCTGTC AGGTACCGCG	60
GGCGTGCACT CTCAGGTCCA GCTTGTCCAG TCTGGGGCTG AAGTCAAGAA ACCT	114

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(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (oligonucleotide)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

TTTTGAATTC TCGAGACCCT GTCCAGGGGC CTGCCTTACC CAGTTTATCC AGGAGCTAGT	60
AAAGATGTAG CCAGAAGCTT TGCAGGAGAC CTTACGGAG CTCCCAGGTT TCTTGACTTC	120
A	121

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (oligonucleotide)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

TTTTGAATTC TCGAGTGGAT GGGAAGGATT GATCCTTCCG ATGGTGAAGT TCACTACAAT	60
CAAGATTTC AAGACCGTGT TACAATTACA GCAGACGAAT CCACCAATAC AGCCTACATG	120
GAACTGAGCA GCCTGAG	137

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (oligonucleotide)

162  
194

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

TTTTTCTAGA GGTTTTAAGG ACTCACCTGA GGAGACTGTG ACCAGGGTTC CTTGGCCCCA	60
GTCAGCAAAC CAGGGCAGAA ATCCTCTTGC ACAGTAATAG ACTGCAGTGT CCTCTGATCT	120
CAGGCTGCTC AGTT	134

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